STIC Biotechnology Systems Branch

RAW SEQUENCE LISTING
ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: _10/785,607A_
Source: _1FW16_
Date Processed by STIC: _7/15/05_

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.
PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:
1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY
FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT MARK SPENCER, TELEPHONE: 571-272-2510; FAX: 571-273-0221

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE <u>CHECKER VERSION 4.2.2 PROGRAM</u>, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:
        http://www.uspto.gov/web/offices/pac/checker/chkrnote.htm

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail. Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom. Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<u><http://www.uspto.gov/ebc/efs/downloads/documents.htm></u> , EFS Submission User Manual - ePAVE)
2. U.S. Postal Service: Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450.
3. Hand Carry, Federal Express, United Parcel Service, or other delivery service (EFFECTIVE 01/14/05): U.S. Patent and Trademark Office, Mail Stop Sequence, Customer Window, Randolph Building, 401 Dulany Street. Alexandria, VA 22314

Revised 01/24/05

Raw Sequence Listing Error Summary

ERROR DETECTED	SUGGESTED CORRECTION	SERIAL NUMBER: _10/985,607A_

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

1_____Wrapped Nucleics Wrapped Aminos
The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor **after** creating it. Please adjust your right margin to .3; this will prevent "wrapping."

2_____Invalid Line Length
The rules require that a line **not exceed** 72 characters in length. This includes white spaces.

3_____Misaligned Amino Numbering
The numbering under each 5th amino acid is misaligned. Do **not** use tab codes between numbers; use **space characters**, instead.

4_____Non-ASCII
The submitted file was **not** saved in ASCII(DOS) text, as **required** by the Sequence Rules. **Please ensure your subsequent submission is saved in ASCII text.**

5_____Variable Length
Sequence(s)_____contain n's or Xaa's representing more than one residue. **Per Sequence Rules, each n or Xaa can only represent a single residue.** Please present the **maximum** number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.

6_____PatentIn 2.0 "bug"
A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) _____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. **This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.**

7_____Skipped Sequences (OLD RULES)
Sequence(s) _____ missing. If intentional, please insert the following lines for **each** skipped sequence:
(2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
(i)   SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
This sequence is intentionally skipped

Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.

8_____Skipped Sequences (NEW RULES)
Sequence(s) _____ missing. If **intentional**, please insert the following lines for **each** skipped sequence.
<210> sequence id number
<400> sequence id number
000

9_____Use of n's or Xaa's (NEW RULES)
Use of n's and/or Xaa's have been detected in the Sequence Listing.
Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.

10_____Invalid <213> Response
Per 1.823 of Sequence Rules, the only **valid** <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is **required** when <213> response is Unknown or is Artificial Sequence

11_____Use of <220>
Sequence(s) _____ missing the <220> "Feature" and associated numeric identifiers and responses. Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32)   (Sec. 1.823 of Sequence Rules)

12_____PatentIn 2.0 "bug"
Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.

13_____ Misuse of n/Xaa
"n" can **only** represent a single <u>nucleotide</u>; "Xaa" can **only** represent a single <u>amino acid</u>

AMC – Biotechnology Systems Branch – 09/09/2003

IFW16

RAW SEQUENCE LISTING   DATE: 07/15/2005
PATENT APPLICATION: US/10/785,607A   TIME: 11:09:25

Input Set : A:\39780-1216R1C1D5 SAVED JULY 7 2005.TXT
Output Set: N:\CRF4\07152005\J785607A.raw

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 4 <110> APPLICANT: Ashkenazi, Avi J.
 5        Fong, Sherman
 6        Goddard, Audrey
 7        Gurney, Austin L.
 8        Napier, Mary A.
 9        Tumas, Daniel
10        Wood, William I.
12 <120> TITLE OF INVENTION: COMPOUNDS, COMPOSITIONS AND METHODS FOR
13        THE TREATMENT OF DISEASES CHARACTERIZED BY A-33 RELATED
14        ANTIGENS
16 <130> FILE REFERENCE: 39780-1216R1C1D5
18 <140> CURRENT APPLICATION NUMBER: US 10/785,607A
19 <141> CURRENT FILING DATE: 2004-02-24
21 <150> PRIOR APPLICATION NUMBER: US 09/953,499
22 <151> PRIOR FILING DATE: 2001-09-14
24 <150> PRIOR APPLICATION NUMBER: US 09/254,465
25 <151> PRIOR FILING DATE: 1999-03-05
27 <150> PRIOR APPLICATION NUMBER: PCT/US98/24855
28 <151> PRIOR FILING DATE: 1998-11-20
30 <150> PRIOR APPLICATION NUMBER: PCT/US98/19437
31 <151> PRIOR FILING DATE: 1998-09-17
33 <160> NUMBER OF SEQ ID NOS: 30
35 <170> SOFTWARE: FastSEQ for Windows Version 4.0
37 <210> SEQ ID NO: 1
38 <211> LENGTH: 299
39 <212> TYPE: PRT
40 <213> ORGANISM: Homo sapiens
42 <400> SEQUENCE: 1
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45 Leu Ala Ile Leu Leu Cys Ser Leu Ala Leu Gly Ser Val Thr Val His
46             20                  25                  30
47 Ser Ser Glu Pro Glu Val Arg Ile Pro Glu Asn Asn Pro Val Lys Leu
48         35                  40                  45
49 Ser Cys Ala Tyr Ser Gly Phe Ser Ser Pro Arg Val Glu Trp Lys Phe
50     50                  55                  60
51 Asp Gln Gly Asp Thr Thr Arg Leu Val Cys Tyr Asn Asn Lys Ile Thr
52 65                  70                  75                  80
53 Ala Ser Tyr Glu Asp Arg Val Thr Phe Leu Pro Thr Gly Ile Thr Phe
54             85                  90                  95
55 Lys Ser Val Thr Arg Glu Asp Thr Gly Thr Tyr Thr Cys Met Val Ser
56             100                 105                 110
57 Glu Glu Gly Gly Asn Ser Tyr Gly Glu Val Lys Val Lys Leu Ile Val
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        RAW SEQUENCE LISTING              DATE: 07/15/2005
        PATENT APPLICATION:  US/10/785,607A    TIME: 11:09:25

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        Output Set: N:\CRF4\07152005\J785607A.raw
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59 Leu Val Pro Pro Ser Lys Pro Thr Val Asn Ile Pro Ser Ser Ala Thr
60      130                 135                 140
61 Ile Gly Asn Arg Ala Val Leu Thr Cys Ser Glu Gln Asp Gly Ser Pro
62 145                 150                 155                 160
63 Pro Ser Glu Tyr Thr Trp Phe Lys Asp Gly Ile Val Met Pro Thr Asn
64                 165                 170                 175
65 Pro Lys Ser Thr Arg Ala Phe Ser Asn Ser Ser Tyr Val Leu Asn Pro
66                 180                 185                 190
67 Thr Thr Gly Glu Leu Val Phe Asp Pro Leu Ser Ala Ser Asp Thr Gly
68                 195                 200                 205
69 Glu Tyr Ser Cys Glu Ala Arg Asn Gly Tyr Gly Thr Pro Met Thr Ser
70      210                 215                 220
71 Asn Ala Val Arg Met Glu Ala Val Glu Arg Asn Val Gly Val Ile Val
72 225                 230                 235                 240
73 Ala Ala Val Leu Val Thr Leu Ile Leu Leu Gly Ile Leu Val Phe Gly
74                 245                 250                 255
75 Ile Trp Phe Ala Tyr Ser Arg Gly His Phe Asp Arg Thr Lys Lys Gly
76                 260                 265                 270
77 Thr Ser Ser Lys Lys Val Ile Tyr Ser Gln Pro Ser Ala Arg Ser Glu
78      275                 280                 285
79 Gly Glu Phe Lys Gln Thr Ser Ser Phe Leu Val
80      290                 295
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84 <211> LENGTH: 321
85 <212> TYPE: PRT
86 <213> ORGANISM: Homo sapiens
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90 1             5                 10                  15
91 Thr Tyr Gly Arg Pro Ile Leu Glu Val Pro Glu Ser Val Thr Gly Pro
92           20                  25                  30
93 Trp Lys Gly Asp Val Asn Leu Pro Cys Thr Tyr Asp Pro Leu Gln Gly
94       35                  40                  45
95 Tyr Thr Gln Val Leu Val Lys Trp Leu Val Gln Arg Gly Ser Asp Pro
96    50                  55                  60
97 Val Thr Ile Phe Leu Arg Asp Ser Ser Gly Asp His Ile Gln Gln Ala
98 65                  70                  75                  80
99 Lys Tyr Gln Gly Arg Leu His Val Ser His Lys Val Pro Gly Asp Val
100               85                  90                  95
101 Ser Leu Gln Leu Ser Thr Leu Glu Met Asp Asp Arg Ser His Tyr Thr
102           100                 105                 110
103 Cys Glu Val Thr Trp Gln Thr Pro Asp Gly Asn Gln Val Val Arg Asp
104       115                 120                 125
105 Lys Ile Thr Glu Leu Arg Val Gln Lys Leu Ser Val Ser Lys Pro Thr
106     130                 135                 140
107 Val Thr Thr Gly Ser Gly Tyr Gly Phe Thr Val Pro Gln Gly Met Arg
108 145                 150                 155                 160
109 Ile Ser Leu Gln Cys Gln Ala Arg Gly Ser Pro Pro Ile Ser Tyr Ile
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```
                    RAW SEQUENCE LISTING              DATE: 07/15/2005
                    PATENT APPLICATION:  US/10/785,607A    TIME: 11:09:25

                    Input Set : A:\39780-1216R1C1D5 SAVED JULY 7 2005.TXT
                    Output Set: N:\CRF4\07152005\J785607A.raw

110                165                170                175
111 Trp Tyr Lys Gln Gln Thr Asn Asn Gln Glu Pro Ile Lys Val Ala Thr
112                180                185                190
113 Leu Ser Thr Leu Leu Phe Lys Pro Ala Val Ile Ala Asp Ser Gly Ser
114            195                200                205
115 Tyr Phe Cys Thr Ala Lys Gly Gln Val Gly Ser Glu Gln His Ser Asp
116     210                215                220
117 Ile Val Lys Phe Val Val Lys Asp Ser Ser Lys Leu Leu Lys Thr Lys
118 225                230                235                240
119 Thr Glu Ala Pro Thr Thr Met Thr Tyr Pro Leu Lys Ala Thr Ser Thr
120                245                250                255
121 Val Lys Gln Ser Trp Asp Trp Thr Thr Asp Met Asp Gly Tyr Leu Gly
122            260                265                270
123 Glu Thr Ser Ala Gly Pro Gly Lys Ser Leu Pro Val Phe Ala Ile Ile
124            275                280                285
125 Leu Ile Ile Ser Leu Cys Cys Met Val Val Phe Thr Met Ala Tyr Ile
126     290                295                300
127 Met Leu Cys Arg Lys Thr Ser Gln Gln Glu His Val Tyr Glu Ala Ala
128 305                310                315                320
129 Arg
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134 <211> LENGTH: 390
135 <212> TYPE: DNA
136 <213> ORGANISM: Artificial Sequence
138 <220> FEATURE:
139 <223> OTHER INFORMATION: Artificial sequence
141 <400> SEQUENCE: 3
142 cttcttgcca actggtatca ccttcaagtc cgtgacacgg gaagacactg ggacatacac 60
143 ttgtatggtc tctgaggaag gcggcaacag ctatggggag gtcaaggtca agctcatcgt 120
144 gcttgtgcct ccatccaagc ctacagttaa catcccctcc tctgccacca ttgggaaccg 180
145 ggcagtgctg acatgctcag aacaagatgg ttccccacct tctgaataca cctggttcaa 240
146 agatgggata gtgatgccta cgaatcccaa aagcacccgt gccttcagca actcttccta 300
147 tgtcctgaat cccacaacag gagagctggt ctttgatccc ctgtcagcct ctgatactgg 360
148 agaatacagc tgtgaggcac ggaatgggta                                  390
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152 <212> TYPE: DNA
153 <213> ORGANISM: Artificial Sequence
155 <220> FEATURE:
156 <223> OTHER INFORMATION: Artificial sequence
158 <400> SEQUENCE: 4
159 tctcagtccc ctcgctgtag tcgcggagct gtgttctgtt tcccaggagt ccttcggcgg 60
160 ctgttgtgct caggtgcgcc tgatcgcgat ggggacaaag gcgcaagctc gagaggaaac 120
161 tgttgtgcct cttcatattg gcgatcctgt tgtgctccct ggcattgggc agtgttacag 180
162 ttgcactctt ctgaacctga agtcagaatt cctgagaata atcctgtgaa gttgtcctgt 240
163 gcctactcgg gctttttctt tccccgtgtg gagtggaagt ttgaccaagg agacaccacc 300
164 agactcgttt gctataataa caagatcaca gcttcctatg aggaccgggt gaccttcttg 360
165 ccaactggta tcaccttcaa gtccgtgaca cgggaagaca ctgggacata cacttgtatg 420
166 gtctctgagg aaggcggcaa cagctatggg gaggtcaagg tcaagctcat cgtgcttgtg 480
```

insufficient explanation - give source of genetic material (see item 11 on Error summary sheet)

same error

```
167 cctccatcca agcctacagt taacatcccc tcctctgcca ccattgggaa ccgggcagtg 540
168 ctgacatgct cagaacaaga tggttcccca ccttctgaat acacctggtt caaagatggg 600
169 atagtgatgc ctacgaatcc caaaagcacc cgtgccttca gcaactcttc ctatgtcctg 660
170 aatcccacaa caggagagct ggtctttgat cccctgtcag cctctgatac tggagaatac 720
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176 <213> ORGANISM: Artificial Sequence
178 <220> FEATURE:
179 <223> OTHER INFORMATION: Artificial sequence
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184 gactcctgat ggcaaccaag tcgtgagaga taagattact gagctccgtg tccagaaact 180
185 ctctgtctcc aagcccacag tgacaactgg cagcggttat ggcttcacgg tgccccaggg 240
186 aatgaggatt agccttcaat gccagggttc ggggttctcc tcccatcagt tatatttggt 300
187 ataagcaaca gactaataac cagggaaccc atcaaagtag caaccctaag taccttactc 360
188 ttcaagcctg cggtgatagc cgactcaggc tcctatttct gcactgccaa gggccaggtt 420
189 ggctctgagc agcacagcga cattgtgaag tttgtggtca aagactcctc aaagctactc 480
190 aagaccaaga ctgaggcacc tacaaccatg acataccct tgaaagcaac atctacagtg 540
191 aagcagtcct gggactggac cactgacatg gatggctacc ttggagagac cagtgctggg 600
192 ccaggaaaga gcctgcctgt ctttgccatc atcctcatca tctccttgtg ctgtatggtg 660
193 gtttttacca tggcctatat catgctctgt cggaagacat cccaacaaga gcatgtctac 720
194 gaagcagcca gggcacatgc cagagaggcc aacgactctg gagaaaccat gagggtggcc 780
195 atcttcgcaa gtggctgctc cagtgatgag ccaacttccc agaatctggg gcaacaacta 840
196 ctctgatgag ccctgcatag gacaggagta ccagatcatc gcccagatca atggcaacta 900
197 cgcccgcctg ctggacacag ttcctctgga ttatgagttt ctggccactg agggcaaaag 960
198 tgtctgttaa aaatgcccca ttaggccagg atctgctgac ataattgcct agtcagtcct 1020
199 tgccttctgc atggccttct tccctgctac ctctcttcct ggatagccca aagtgtccgc 1080
200 ctaccaacac tggagccgct gggagtcact ggctttgccc tggaatttgc cagatgcatc 1140
201 tcaagtaagc cagctgctgg atttggctct gggcccttct agtatctctg ccgggggctt 1200
202 ctggtactcc tctctaaata ccagagggaa gatgcccata gcactaggac ttggtcatca 1260
203 tgcctacaga cactattcaa ctttggcatc ttgccaccag aagacccgag gggaggctca 1320
204 gctctgccag ctcagaggac cagctatatc caggatcatt tctctttctt cagggccaga 1380
205 cagcttttaa ttgaaattgt tatttcacag gccagggttc agttctgctc ctccactata 1440
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207 aaa                                                             1503
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210 <211> LENGTH: 319
211 <212> TYPE: PRT
212 <213> ORGANISM: Homo sapiens
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216  1               5                  10                  15
217 Val Thr Val Asp Ala Ile Ser Val Glu Thr Pro Gln Asp Val Leu Arg
218              20                  25                  30
219 Ala Ser Gln Gly Lys Ser Val Thr Leu Pro Cys Thr Tyr His Thr Ser
220          35                  40                  45
```

This error appears in subsequent sequences, too. [handwritten annotation]

:   ˵

```
221 Thr Ser Ser Arg Glu Gly Leu Ile Gln Trp Asp Lys Leu Leu Leu Thr
222     50                  55                  60
223 His Thr Glu Arg Val Val Ile Trp Pro Phe Ser Asn Lys Asn Tyr Ile
224 65                      70                  75                  80
225 His Gly Glu Leu Tyr Lys Asn Arg Val Ser Ile Ser Asn Asn Ala Glu
226                     85                  90                  95
227 Gln Ser Asp Ala Ser Ile Thr Ile Asp Gln Leu Thr Met Ala Asp Asn
228             100                 105                 110
229 Gly Thr Tyr Glu Cys Ser Val Ser Leu Met Ser Asp Leu Glu Gly Asn
230             115                 120                 125
231 Thr Lys Ser Arg Val Arg Leu Leu Val Leu Val Pro Pro Ser Lys Pro
232     130                 135                 140
233 Glu Cys Gly Ile Glu Gly Glu Thr Ile Ile Gly Asn Asn Ile Gln Leu
234 145                 150                 155                 160
235 Thr Cys Gln Ser Lys Glu Gly Ser Pro Thr Pro Gln Tyr Ser Trp Lys
236             165                 170                 175
237 Arg Tyr Asn Ile Leu Asn Gln Glu Gln Pro Leu Ala Gln Pro Ala Ser
238             180                 185                 190
239 Gly Gln Pro Val Ser Leu Lys Asn Ile Ser Thr Asp Thr Ser Gly Tyr
240             195                 200                 205
241 Tyr Ile Cys Thr Ser Ser Asn Glu Glu Gly Thr Gln Phe Cys Asn Ile
242     210                 215                 220
243 Thr Val Ala Val Arg Ser Pro Ser Met Asn Val Ala Leu Tyr Val Gly
244 225                 230                 235                 240
245 Ile Ala Val Gly Val Val Ala Ala Leu Ile Ile Ile Gly Ile Ile Ile
246             245                 250                 255
247 Tyr Cys Cys Cys Cys Arg Gly Lys Asp Asp Asn Thr Glu Asp Lys Glu
248             260                 265                 270
249 Asp Ala Arg Pro Asn Arg Glu Ala Tyr Glu Glu Pro Pro Glu Gln Leu
250         275                 280                 285
251 Arg Glu Leu Ser Arg Glu Arg Glu Glu Glu Asp Asp Tyr Arg Gln Glu
252     290                 295                 300
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259 <212> TYPE: DNA
260 <213> ORGANISM: Homo sapiens
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265 ggggatctta ctgggcctgc tactcctggg gcacctaaca gtggacactt atggccgtcc 180
266 catcctggaa gtgccagaga gtgtaacagg accttggaaa ggggatgtga atcttccctg 240
267 cacctatgac cccctgcaag gctacacccca agtcttggtg aagtggctgg tacaacgtgg 300
268 ctcagaccct gtcaccatct ttctacgtga ctcttctgga gaccatatcc agcaggcaaa 360
269 gtaccagggc cgcctgcatg tgagccacaa ggttccagga gatgtatccc tccaattgag 420
270 caccctggag atggatgacc ggagccacta cacgtgtgaa gtcacctggc agactcctga 480
271 tggcaaccaa gtcgtgagag ataagattac tgagctccgt gtccagaaac tctctgtctc 540
272 caagcccaca gtgacaactg gcagcggtta tggcttcacg gtgccccagg gaatgaggat 600
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VERIFICATION SUMMARY   DATE: 07/15/2005
PATENT APPLICATION: **US/10/785,607A**   TIME: 11:09:26

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